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|--------------|---------|---|
| NEWS         | 1       | Web Page URLs for STN Seminar Schedule - N. America   |
| NEWS         | 2       | "Ask CAS" for self-help around the clock  |
| NEWS         | 3       | May 12 EXTEND option available in structure searching   |
| NEWS         | 4       | May 12 Polymer links for the POLYLINK command completed in REGISTRY   |
| NEWS         | 5       | May 27 New UPM (Update Code Maximum) field for more efficient patent SDIs in CApplus  |
| NEWS         | 6       | May 27 CApplus super roles and document types searchable in REGISTRY  |
| NEWS         | 7       | Jun 28 Additional enzyme-catalyzed reactions added to CASREACT  |
| NEWS         | 8       | Jun 28 ANTE, AQUALINE, BIOENG, CIVILENG, ENVIROENG, MECHENG, and WATER from CSA now available on STN(R)                                     |
| NEWS         | 9       | Jul 12 BEILSTEIN enhanced with new display and select options, resulting in a closer connection to BABS                                     |
| NEWS         | 10      | Jul 30 BEILSTEIN on STN workshop to be held August 24 in conjunction with the 228th ACS National Meeting                                    |
| NEWS         | 11      | AUG 02 IFIPAT/IFIUDB/IFICDB reloaded with new search and display fields   |
| NEWS         | 12      | AUG 02 CApplus and CA patent records enhanced with European and Japan Patent Office Classifications   |
| NEWS         | 13      | AUG 02 STN User Update to be held August 22 in conjunction with the 228th ACS National Meeting  |
| NEWS         | 14      | AUG 02 The Analysis Edition of STN Express with Discover! (Version 7.01 for Windows) now available  |
| NEWS         | 15      | AUG 04 Pricing for the Save Answers for SciFinder Wizard within STN Express with Discover! will change September 1, 2004                    |
| NEWS EXPRESS | JULY 30 | CURRENT WINDOWS VERSION IS V7.01, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 11 AUGUST 2004 |
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FILE 'HOME' ENTERED AT 10:16:32 ON 17 AUG 2004

=> FIL STNGUIDE

| COST IN U.S. DOLLARS | SINCE FILE ENTRY | TOTAL SESSION |
|----------------------|------------------|---------------|
| FULL ESTIMATED COST  | 0.42             | 0.42          |

FILE 'STNGUIDE' ENTERED AT 10:17:29 ON 17 AUG 2004  
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FILE CONTAINS CURRENT INFORMATION.  
 LAST RELOADED: Aug 6, 2004 (20040806/UP).

| COST IN U.S. DOLLARS | SINCE FILE ENTRY | TOTAL SESSION |
|----------------------|------------------|---------------|
| FULL ESTIMATED COST  | 0.06             | 0.48          |

FILE 'HOME' ENTERED AT 10:17:52 ON 17 AUG 2004

| COST IN U.S. DOLLARS | SINCE FILE ENTRY | TOTAL SESSION |
|----------------------|------------------|---------------|
| FULL ESTIMATED COST  | 0.21             | 0.69          |

FILE 'MEDLINE' ENTERED AT 10:17:59 ON 17 AUG 2004

FILE LAST UPDATED: 14 AUG 2004 (20040814/UP). FILE COVERS 1951 TO DATE.

On February 29, 2004, the 2004 MeSH terms were loaded. See HELP RLOAD for details. OLD MEDLINE now back to 1951.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2004 vocabulary. See <http://www.nlm.nih.gov/mesh/> and [http://www.nlm.nih.gov/pubs/techbull/nd03/nd03\\_mesh.html](http://www.nlm.nih.gov/pubs/techbull/nd03/nd03_mesh.html) for a description of changes.

This file contains CAS Registry Numbers for easy and accurate substance identification.

```
=> s acropora+NT/CT
'ACROPORA' NOT IN RELATIONSHIP FILE
RELATIONSHIP CODE 'NT' IGNORED
L1          0 ACROPORA+NT/CT (1 TERM)
```

```
=> s Montipora+NT/CT
'MONTIPORA' NOT IN RELATIONSHIP FILE
RELATIONSHIP CODE 'NT' IGNORED
L2          0 MONTIPORA+NT/CT (1 TERM)
```

```
=> s Acropora?
L3          75 ACROPORA?
```

```
=> s Montipora?
L4          20 MONTIPORA?
```

```
=> s l3 and DNA
          756893 DNA
L5          28 L3 AND DNA
```

```
=> s l4 and DNA
          756893 DNA
L6          1 L4 AND DNA
```

```
=> d l6 ti abs ibib tot
```

L6 ANSWER 1 OF 1 MEDLINE on STN  
 TI Specificity of a model cnidarian-dinoflagellate symbiosis.  
 AB To understand the flexibility of symbiotic associations in coral reefs, we investigated the specificity of the Aiptasia (cf. insignis)-Symbiodinium association in the laboratory by rendering the anemones aposymbiotic and inoculating them with different isolates of SYMBIODINIUM: Infective algal symbionts were monitored over 3 months by re-isolation and identification using denaturing-gradient gel electrophoresis and sequence comparison of their amplified 18S rRNA hypervariable V1 + V2 gene region. Despite similarity in their external morphology, the algal isolates differed in their infectivity towards the host. Within days of single-isolate inoculation, aposymbiotic anemones formed associations with fresh or cultured isolates (clade B) from the anemones Aiptasia sp. or A. tagetes, respectively. They associated to a limited extent with cultured isolates (clade A) from the tridacnids Tridacna crocea or Hippopus hippopus, and not at all with a cultured isolate (clade C) from the stony coral *Montipora verrucosa*, nor with a free-living isolate (clade A) from subtidal sands. Aposymbiotic anemones inoculated with a mixture of all isolates had only the anemone taxon as their detectable symbionts. Re-inoculation of induced symbioses with a mixture of all isolates and incubation with wild anemones showed that the initial induced symbioses with the anemone taxon were stable. Anemones originally infected with tridacnid isolates either additionally acquired the anemone taxon or had the former outgrown by the latter. These results demonstrate the presence of a host-symbiont recognition mechanism, and possibly competition among potential algal symbionts in the Aiptasia-Symbiodinium association. Here we present a method that may be useful in monitoring the algal population dynamics in symbiotic corals in the field, along with an efficient method of rendering Aiptasia aposymbiotic for further laboratory investigation of Aiptasia-Symbiodinium symbioses.

ACCESSION NUMBER: 2002109855 MEDLINE  
 DOCUMENT NUMBER: PubMed ID: 11842017  
 TITLE: Specificity of a model cnidarian-dinoflagellate symbiosis.  
 AUTHOR: Belda-Baillie Carmen A; Baillie Brett K; Maruyama Tadashi  
 CORPORATE SOURCE: Marine Biotechnology Institute Co., Ltd., Kamaishi Laboratories, Heita, Kamaishi City, Iwate 026-0001, Japan.. carmen.baillie@csiro.au  
 SOURCE: Biological bulletin, (2002 Feb) 202 (1) 74-85.  
 Journal code: 2984727R. ISSN: 0006-3185.  
 PUB. COUNTRY: United States  
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
 LANGUAGE: English  
 FILE SEGMENT: Priority Journals  
 ENTRY MONTH: 200204  
 ENTRY DATE: Entered STN: 20020214  
 Last Updated on STN: 20020430  
 Entered Medline: 20020429

=> d his

(FILE 'HOME' ENTERED AT 10:16:32 ON 17 AUG 2004)

FILE 'STNGUIDE' ENTERED AT 10:17:29 ON 17 AUG 2004

FILE 'HOME' ENTERED AT 10:17:52 ON 17 AUG 2004

FILE 'MEDLINE' ENTERED AT 10:17:59 ON 17 AUG 2004

L1 0 S ACROPORA+NT/CT  
 L2 0 S MONTIPORA+NT/CT  
 L3 75 S ACROPORA?  
 L4 20 S MONTIPORA?  
 L5 28 S L3 AND DNA

=> d 15 ti abs ibib tot

L5 ANSWER 1 OF 28 MEDLINE on STN

TI A deep-sea slant on the molecular phylogeny of the Scleractinia.

AB Lophelia pertusa and Madrepora oculata are azooxanthellate corals with nearly cosmopolitan distributions. They form cold-water reefs in the upper bathyal zone on continental margins and offshore banks [A.D. Rogers, Int. Rev. Hydrobiol. 84 (1999) 315]. Lophelia is classified in the family Caryophylliidae and Madrepora in the family Oculinidae, both on the basis of skeletal morphology. Recent molecular studies of the scleractinians have given a new insight into the evolutionary history of this group. This study was aimed at clarifying the phylogenetic relationships of Lophelia and Madrepora, through the analysis of partial sequences of the mitochondrial 16S rDNA. Sequences were obtained for samples of L. pertusa collected in the northeast Atlantic and off Brazil, M. oculata, four other deep-sea and eight tropical coral species from the Reunion island in the Indian Ocean. The sequences were aligned with 69 homologous sequences of Scleractinia. Maximum parsimony and Bayesian analyses support previously published molecular topologies. The two specimens of L. pertusa grouped with two caryophylliids, confirming the existing classification of the species, but the large genetic distance between the two Lophelia samples suggests that these populations are genetically isolated from one another. M. oculata did not cluster with oculinids, but formed a monotypic clade lying between the families Pocilloporidae and Caryophylliidae. Phylogenetic analysis also suggested cryptic speciation within the tropical taxa Pocillopora meandriana and possibly **Acropora humilis**.

ACCESSION NUMBER: 2004130206 MEDLINE

DOCUMENT NUMBER: PubMed ID: 15022767

TITLE: A deep-sea slant on the molecular phylogeny of the Scleractinia.

AUTHOR: Le Goff-Vitry M C; Rogers A D; Baglow D

CORPORATE SOURCE: School of Ocean and Earth Science, University of Southampton, Southampton Oceanography Centre, European Way, Southampton SO14 3ZH, UK.. mclg@soc.soton.ac.uk

SOURCE: Molecular phylogenetics and evolution, (2004 Jan) 30 (1) 167-77.

Journal code: 9304400. ISSN: 1055-7903.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200405

ENTRY DATE: Entered STN: 20040317

Last Updated on STN: 20040510

Entered Medline: 20040507

L5 ANSWER 2 OF 28 MEDLINE on STN

TI Geographic and habitat partitioning of genetically distinct zooxanthellae (Symbiodinium) in **Acropora** corals on the Great Barrier Reef.

AB Intra- and intercolony diversity and distribution of zooxanthellae in acroporid corals is largely uncharted. In this study, two molecular methods were applied to determine the distribution of zooxanthellae in the branching corals **Acropora tenuis** and *A. valida* at several reef locations in the central section of the Great Barrier Reef. Sun-exposed and shaded parts of all colonies were examined. Single-stranded conformational polymorphism analysis showed that individual colonies of *A. tenuis* at two locations harbour two strains of Symbiodinium belonging to clade C (C1 and C2), whereas conspecific colonies at two other reefs harboured a single zooxanthella strain. *A. valida* was found to simultaneously harbour strains belonging to two distinct phylogenetic clades (C and D) at all locations sampled. A novel method with improved

sensitivity (quantitative polymerase chain reaction using Taqman fluorogenic probes) was used to map the relative abundance distribution of the two zooxanthella clades. At two of the five sampling locations both coral species were collected. At these two locations, composition of the zooxanthella communities showed the same pattern in both coral species, i.e. correlation with ambient light in Pioneer Bay and an absence thereof in Nelly Bay. The results show that the distribution of genetically distinct zooxanthellae is correlated with light regime and possibly temperature in some (but not all) colonies of *A. tenuis* and *A. valida* and at some reef locations, which we interpret as acclimation to local environmental conditions.

ACCESSION NUMBER: 2003600218 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 14629362  
TITLE: Geographic and habitat partitioning of genetically distinct zooxanthellae (Symbiodinium) in **Acropora** corals on the Great Barrier Reef.  
AUTHOR: Ulstrup K E; Van Oppen M J H  
CORPORATE SOURCE: Department of Phycology, Botanical Institute, University of Copenhagen, Copenhagen, Denmark.  
SOURCE: Molecular ecology, (2003 Dec) 12 (12) 3477-84.  
Journal code: 9214478. ISSN: 0962-1083.  
PUB. COUNTRY: England: United Kingdom  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 200401  
ENTRY DATE: Entered STN: 20031220  
Last Updated on STN: 20040129  
Entered Medline: 20040128

L5 ANSWER 3 OF 28 MEDLINE on STN

TI Unexpected patterns of genetic structuring among locations but not colour morphs in **Acropora** nasuta (Cnidaria; Scleractinia).

AB Symbiotic relationships have contributed greatly to the evolution and maintenance of biological diversity. On the Great Barrier Reef, species of obligate coral-dwelling fishes (genus *Gobiodon*) coexist by selectively recruiting to colonies of **Acropora** nasuta that differ in branch-tip colour. In this study, we investigate genetic variability among sympatric populations of two colour morphs of *A. nasuta* ('blue-tip' and 'brown-tip') living in symbiosis with two fish species, *Gobiodon histrio* and *G. quinquestrigatus*, respectively, to determine whether gobies are selecting between intraspecific colour polymorphisms or cryptic coral species. We also examine genetic differentiation among coral populations containing both these colour morphs that are separated by metres between local sites, tens of kilometres across the continental shelf and hundreds of kilometres along the Great Barrier Reef. We use three nuclear DNA loci, two of which we present here for the first time for **Acropora**. No significant genetic differentiation was detected between sympatric colour morphs at these three loci. Hence, symbiotic gobies are selecting among colour morphs of *A. nasuta*, rather than cryptic species. Significant genetic geographical structuring was observed among populations, independent of colour, at regional (i.e. latitudinal separation by < 500 km) and cross-shelf (< 50 km) scales, alongside relative homogeneity between local populations on within reef scales (< 5 km). This contrasts with the reported absence of large-scale genetic structuring in *A. valida*, which is a member of the same species group as *A. nasuta*. Apparent differences in biogeographical structuring between species within the *A. nasuta* group emphasize the need for comparative sampling across both spatial (i.e. within reefs, between reefs and between regions) and taxonomic scales (i.e. within and between closely related species).

ACCESSION NUMBER: 2003575688 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 14653784  
TITLE: Unexpected patterns of genetic structuring among locations

but not colour morphs in **Acropora nasuta**  
(Cnidaria; Scleractinia).

AUTHOR: Mackenzie J B; Munday P L; Willis B L; Miller D J; van Oppen M J H

CORPORATE SOURCE: Marine Biology and Aquaculture, and Biochemistry and, Molecular Biology, James Cook University, Townsville, Australia.

SOURCE: Molecular ecology, (2004 Jan) 13 (1) 9-20.  
Journal code: 9214478. ISSN: 0962-1083.

PUB. COUNTRY: England: United Kingdom

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200402

ENTRY DATE: Entered STN: 20031216  
Last Updated on STN: 20040221  
Entered Medline: 20040220

L5 ANSWER 4 OF 28 MEDLINE on STN

TI Mutational analysis of the **Acropora millepora** PaxD paired domain highlights the importance of the linker region for **DNA** binding.

AB Pax transcription factors are found in animals, from simple sponges to insects and vertebrates. The defining feature of Pax proteins is the **DNA**-binding paired domain (PD), which consists of two helix-turn-helix subdomains, joined with a linker region. Despite high specificity in vivo, the paired domains of different Pax proteins bind similar consensus **DNA** sequences in vitro. Using bandshift techniques, we show here that the paired domain of the **Acropora millepora** PaxD protein, which unambiguously belongs to the Pax3/7 group, does not bind to three defined paired domain-binding sites. Domain swapping experiments and site-directed mutagenesis identified two amino acid residues in the linker region of the paired domain as critical to **DNA** binding; G70 and S71 are highly conserved in Pax proteins, but differ in PaxD (L70 and N71). The PaxD data thus highlight the importance of the linker region, and particularly G70 and S71, in **DNA** binding by Pax proteins.

ACCESSION NUMBER: 2003519437 MEDLINE

DOCUMENT NUMBER: PubMed ID: 14597391

TITLE: Mutational analysis of the **Acropora millepora** PaxD paired domain highlights the importance of the linker region for **DNA** binding.

AUTHOR: Nordstrom Karin; Scholten Ingo; Nordstrom Johanna; Larhammar Dan; Miller David

CORPORATE SOURCE: Department of Neuroscience, Pharmacology, Uppsala University, Box 593, Uppsala 751 24, Sweden..  
Karin.Nordstrom@cob.lu.se

SOURCE: Gene, (2003 Nov 27) 320 81-7.  
Journal code: 7706761. ISSN: 0378-1119.

PUB. COUNTRY: Netherlands

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200401

ENTRY DATE: Entered STN: 20031105  
Last Updated on STN: 20040128  
Entered Medline: 20040127

L5 ANSWER 5 OF 28 MEDLINE on STN

TI **DNA**-binding characteristics of cnidarian Pax-C and Pax-B proteins in vivo and in vitro: no simple relationship with the Pax-6 and Pax-2/5/8 classes.

AB Cnidarians are the simplest animals in which distinct eyes are present. We have previously suggested that cnidarian Pax-Cam might represent a precursor of the Pax-6 class. Here we show that when expressed in

Drosophila imaginal discs, Pax-Cam chimeric proteins containing the C-terminal region of EY were capable of eye induction and driving expression of a reporter gene under the control of a known EY target (the sine oculis gene). Whilst these results are consistent with a Pax-6-like function for Pax-Cam, in band shift experiments we were unable to distinguish the DNA-binding behaviour of the Pax-Cam Paired domain from that of a second **Acropora** Pax protein, Pax-Bam. The ability of a Pax-Bam/EY chimera to also induce eye formation in leg imaginal discs, together with the in vitro data, cast doubt on previously assumed direct relationships between cnidarian Pax genes and the Pax-6 and Pax-2/5/8 classes of bilateral animals.

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ACCESSION NUMBER: 2003447306 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 14508814  
TITLE: DNA-binding characteristics of cnidarian Pax-C and Pax-B proteins in vivo and in vitro: no simple relationship with the Pax-6 and Pax-2/5/8 classes.  
AUTHOR: Plaza Serge; De Jong Danielle M; Gehring Walter J; Miller David J  
CORPORATE SOURCE: Biozentrum, University of Basel, CH-4056 Basel, Switzerland.  
SOURCE: Journal of experimental zoology. Part B. Molecular and developmental evolution, (2003 Oct 15) 299 (1) 26-35. Journal code: 101168228.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 200312  
ENTRY DATE: Entered STN: 20030926  
Last Updated on STN: 20031218  
Entered Medline: 20031204

L5 ANSWER 6 OF 28 MEDLINE on STN

TI Pseudogenes contribute to the extreme diversity of nuclear ribosomal DNA in the hard coral **Acropora**.

AB One characteristic of Indo-Pacific **Acropora** spp. is extremely high diversity in rDNA sequences at both the species and individual levels. In order to test the hypothesis that pseudogenes may contribute to this diversity, three kinds of analyses were conducted. First, for *A. millepora* (the species containing the most diverse suite of rDNA types), RT-PCR was used to determine which 5.8S rDNA types are expressed. Second, as previous studies have indicated that interspecific hybridization has occurred in the genus **Acropora** and silencing of rDNA loci via nucleolar dominance has been shown in some cases to involve methylation, patterns of variation were examined at methylation-susceptible sites. Third, patterns of substitution at conserved sites (including those that are likely to contribute to secondary structure in rRNA) in the 5.8S rDNA were examined. These analyses consistently indicated that one rDNA sequence type present in a broad range of Indo-Pacific **Acropora** species is likely to consist predominantly of pseudogenes. Patterns of variation also suggest that species may differ with respect to which rDNA sequence types have been silenced and which are active. These pseudogenes are likely to have arisen as a consequence of the introduction of highly divergent rDNA types into single genomes by interspecific hybridization events, and we attribute the extreme rDNA diversity characteristic of many **Acropora** species to both the independent evolution of these silenced rDNA types and to the suppressive effects of high sequence diversity on homogenization processes acting on functional loci.

ACCESSION NUMBER: 2003278260 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 12777522  
TITLE: Pseudogenes contribute to the extreme diversity of nuclear ribosomal DNA in the hard coral **Acropora**

AUTHOR: Marquez Luis M; Miller David J; MacKenzie Jason B; Van Oppen Madeleine J H  
CORPORATE SOURCE: Biochemistry and Molecular Biology, James Cook University, Townsville, Queensland, Australia.  
SOURCE: Molecular biology and evolution, (2003 Jul) 20 (7) 1077-86. Journal code: 8501455. ISSN: 0737-4038.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 200403  
ENTRY DATE: Entered STN: 20030614  
Last Updated on STN: 20040306  
Entered Medline: 20040305

L5 ANSWER 7 OF 28 MEDLINE on STN

TI A DM domain protein from a coral, **Acropora** millepora, homologous to proteins important for sex determination.

AB The identification and functional studies of DM domain-containing proteins Doublesex, MAB-3, and DMRT1 indicated that flies, nematodes, and humans share at least some of the molecular mechanisms of sex determination. We identified a gene, AmDM1, from the coral **Acropora** millepora that encodes a homologous DM domain-containing protein. Molecular analyses show that the AmDM1 primary transcript is processed to generate four different messenger RNAs. Alternative use of two polyadenylation sites produces transcripts that vary only in the 3' untranslated regions, whereas alternative splicing generates transcripts with and without the region coding for the DM domain. All the transcripts include a second motif, the DMA domain, which is found in a number of other proteins containing a DM domain. Hermaphroditic *A. millepora* differentiates sexual cells seasonally before the spring spawn, and Northern blot analysis shows that the AmDM1 transcripts are present at higher levels during sexual differentiation. The non-DM domain-containing messages are also present at significant levels in late embryos, but DM domain transcripts are extremely rare at this stage. These data suggest that the association of DM domain proteins and sexual determination or differentiation predates the separation of the Cnidaria from the rest of the Metazoa.

ACCESSION NUMBER: 2003230931 MEDLINE

DOCUMENT NUMBER: PubMed ID: 12752764

TITLE: A DM domain protein from a coral, **Acropora** millepora, homologous to proteins important for sex determination.

AUTHOR: Miller Steven W; Hayward David C; Bunch Thomas A; Miller David J; Ball Eldon E; Bardwell Vivian J; Zarkower David; Brower Danny L

CORPORATE SOURCE: Departments of Molecular and Cellular Biology and Biochemistry, University of Arizona, Tucson, AZ 85721, USA.

CONTRACT NUMBER: GM42474 (NIGMS)  
GM59152 (NIGMS)

SOURCE: Evolution & development, (2003 May-Jun) 5 (3) 251-8. Journal code: 100883432. ISSN: 1520-541X.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200312

ENTRY DATE: Entered STN: 20030520

Last Updated on STN: 20031230

Entered Medline: 20031229

L5 ANSWER 8 OF 28 MEDLINE on STN

TI Characterizing stress gene expression in reef-building corals exposed to the mosquitoside dibrom.

AB We characterize two genes expressed in **Acropora** cervicornis upon

*Good date*



exposure to 0.5 microg/l of dibrom, a pesticide used for mosquito control in the Florida Keys. Fragments of these genes were isolated, sequenced, and developed into chemiluminescent probes for Northern slot blots. Expression of target transcripts was detected in corals exposed to a variety of stressors including organophosphates, organochlorines, heavy metals, naphthalene, and temperature. Within the context of stressors examined, the D25 probe demonstrates toxicant and concentration specificity for organophosphates, whereas the D50 probe had broader specificity, detecting transcripts in corals exposed to dibrom, naphthalene, and temperature stress. After characterizing specificity in the lab, these probes were used on field samples taken from the Florida Keys. Both probes detected their targets in samples taken from the upper Florida Keys in August 2000. Preliminary search of sequence databases suggest similarity exists between D25 and a thioesterase.

ACCESSION NUMBER: 2003016735 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 12523519  
TITLE: Characterizing stress gene expression in reef-building corals exposed to the mosquitocide dibrom.  
AUTHOR: Morgan Michael B; Snell Terry W  
CORPORATE SOURCE: Georgia Institute of Technology, School of Biology, Atlanta, GA 30332-0230, USA.. biommm@langate.gsu.edu  
SOURCE: Marine pollution bulletin, (2002 Nov) 44 (11) 1206-18. Journal code: 0260231. ISSN: 0025-326X.  
PUB. COUNTRY: England: United Kingdom  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
OTHER SOURCE: GENBANK-BI534456; GENBANK-BI534457; GENBANK-BI534458; GENBANK-BI534459  
ENTRY MONTH: 200305  
ENTRY DATE: Entered STN: 20030114  
Last Updated on STN: 20030502  
Entered Medline: 20030501

L5 ANSWER 9 OF 28 MEDLINE on STN

TI The mitochondrial genome of **Acropora tenuis** (Cnidaria; Scleractinia) contains a large group I intron and a candidate control region.

AB The complete nucleotide sequence of the mitochondrial genome of the coral **Acropora tenuis** has been determined. The 18,338 bp A. tenuis mitochondrial genome contains the standard metazoan complement of 13 protein-coding and two rRNA genes, but only the same two tRNA genes (trnM and trnW) as are present in the mtDNA of the sea anemone, Metridium senile. The A. tenuis nad5 gene is interrupted by a large group I intron which contains ten protein-coding genes and rns; M. senile has an intron at the same position but this contains only two protein-coding genes. Despite the large distance (about 11.5 kb) between the 5'-exon and 3'-exon boundaries, the A. tenuis nad5 gene is functional, as we were able to RT-PCR across the predicted intron splice site using total RNA from A. tenuis. As in M. senile, all of the genes in the A. tenuis mt genome have the same orientation, but their organization is completely different in these two zoantharians: The only common gene boundaries are those at each end of the group I intron and between trnM and rnl. Finally, we provide evidence that the rns-cox3 intergenic region in A. tenuis may correspond to the mitochondrial control region of higher animals. This region contains repetitive elements, and has the potential to form secondary structures of the type characteristic of vertebrate D-loops. Comparisons between a wide range of **Acropora** species showed that a long hairpin predicted in rns-cox3 is phylogenetically conserved, and allowed the tentative identification of conserved sequence blocks.

ACCESSION NUMBER: 2002409827 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 12165838  
TITLE: The mitochondrial genome of **Acropora tenuis** (Cnidaria; Scleractinia) contains a large group I intron

and a candidate control region.

AUTHOR: van Oppen Madeleine J H; Catmull Julian; McDonald Brenda J; Hislop Nikki R; Hagerman Paul J; Miller David J

CORPORATE SOURCE: Biochemistry and Molecular Biology, James Cook University, Townsville, Queensland 4811, Australia.

CONTRACT NUMBER: GM35305 (NIGMS)

SOURCE: Journal of molecular evolution, (2002 Jul) 55 (1) 1-13.  
Journal code: 0360051. ISSN: 0022-2844.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200302

ENTRY DATE: Entered STN: 20020808  
Last Updated on STN: 20030205  
Entered Medline: 20030204

L5 ANSWER 10 OF 28 MEDLINE on STN

TI Spawning times, reproductive compatibilities and genetic structuring in the **Acropora** aspera group: evidence for natural hybridization and semi-permeable species boundaries in corals.

AB Species boundaries among five sympatric coral species of the Indo-Pacific **Acropora** aspera group were examined by a combination of in vitro breeding trials, comparisons of spawning times and DNA sequence analysis of ribosomal DNA internal transcribed spacer (rDNA ITS) and 5.8S regions. The breeding trials showed that reproductive compatibility exists between at least some colonies of all the species pairs tested, suggesting a large potential for natural hybridization and introgression. The **Acropora** ITS regions exhibited extremely high levels of variability (up to approximately 62% for ITS1, approximately 11% for 5.8S and approximately 43% for ITS2), but most of the variation was shared among four of the five species, *A. millepora*, *A. papillare*, *A. pulchra* and *A. spathulata*, consistent with extensive introgression. Phylogenetic analyses did not resolve these four species as distinct clusters across a wide biogeographic region stretching from the southern Great Barrier Reef to Papua New Guinea. However, most colonies of the fifth species, *A. aspera*, constituted a distinct clade in phylogenetic analyses. This is consistent with our observations of a semi-permeable temporal barrier involving differences in spawning times between this and the other four species. Although the majority of colonies of all five species generally spawned within 90 min of each other, in two out of four years, gametes were absent prior to mass spawning episodes from at least some *A. aspera* colonies. Hence, our data suggest that transient reproductive barriers may be the result of year-to-year variation in the date of spawning and that this difference in spawning time contributes to the genetic structure detected among **Acropora** species in this group. Occasional leakage through the reproductive barrier was confirmed by the observation of *A. aspera* x *A. pulchra* F1 hybrids, identified based on additivity of ITS sequences.

ACCESSION NUMBER: 2002396524 MEDLINE

DOCUMENT NUMBER: PubMed ID: 12144658

TITLE: Spawning times, reproductive compatibilities and genetic structuring in the **Acropora** aspera group: evidence for natural hybridization and semi-permeable species boundaries in corals.

AUTHOR: Van Oppen Madeleine J H; Willis Bette L; Van Rheede Teun; Miller David J

CORPORATE SOURCE: Biochemistry and Molecular Biology, James Cook University, Townsville 4811, Australia.

SOURCE: Molecular ecology, (2002 Aug) 11 (8) 1363-76.  
Journal code: 9214478. ISSN: 0962-1083.

PUB. COUNTRY: England: United Kingdom

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals  
ENTRY MONTH: 200212  
ENTRY DATE: Entered STN: 20020730  
Last Updated on STN: 20021217  
Entered Medline: 20021209

L5 ANSWER 11 OF 28 MEDLINE on STN

TI The highly cross-fertile coral species, **Acropora** hyacinthus and **Acropora** cytherea, constitute statistically distinguishable lineages.

AB A major challenge for understanding the evolutionary genetics of mass-spawning corals is to explain the maintenance of discrete morphospecies in view of high rates of interspecific fertilization in vitro and nonmonophyletic patterns in molecular phylogenies. In this study, we focused on **Acropora** cytherea and A. hyacinthus, which have one of the highest potentials for interspecific fertilization. Using sequences of a nuclear intron, we performed phylogenetic and nested clade analyses (NCA). Both species were polyphyletic in molecular phylogenies, but the NCA indicated that they constitute statistically distinguishable lineages. Phylogenetic analysis using an intergenic region of the mitochondrial **DNA** (mtDNA), was inconclusive because of low levels of variability in this marker. The position of these two species differed between the nuclear **DNA** (nDNA) and mtDNA phylogenies and was also at odds with a cladistic analysis based on morphology. We conclude that despite the potential for high levels of hybridization and introgression, A. cytherea and A. hyacinthus constitute statistically distinguishable lineages and their taxonomic status is consistent with the cohesion species concept.

ACCESSION NUMBER: 2002396522 MEDLINE

DOCUMENT NUMBER: PubMed ID: 12144656

TITLE: The highly cross-fertile coral species, **Acropora** hyacinthus and **Acropora** cytherea, constitute statistically distinguishable lineages.

AUTHOR: Marquez L M; Van Oppen M J H; Willis B L; Reyes A; Miller D J

CORPORATE SOURCE: Biochemistry and Molecular Biology and Marine Biology, James Cook University, Townsville 4811, Australia..  
lmarquez@ivic.vu

SOURCE: Molecular ecology, (2002 Aug) 11 (8) 1339-49.  
Journal code: 9214478. ISSN: 0962-1083.

PUB. COUNTRY: England: United Kingdom

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200212

ENTRY DATE: Entered STN: 20020730  
Last Updated on STN: 20021217  
Entered Medline: 20021209

L5 ANSWER 12 OF 28 MEDLINE on STN

TI Coral development: from classical embryology to molecular control.

AB The phylum Cnidaria is the closest outgroup to the triploblastic metazoans and as such offers unique insights into evolutionary questions at several levels. In the post-genomic era, a knowledge of the gene complement of representative cnidarians will be important for understanding the relationship between the expansion of gene families and the evolution of morphological complexity among more highly evolved metazoans. Studies of cnidarian development and its molecular control will provide information about the origins of the major bilaterian body axes, the origin of the third tissue layer, the mesoderm, and the evolution of nervous system patterning. We are studying the cnidarian **Acropora** millepora, a reef building scleractinian coral, and a member of the basal cnidarian class, the Anthozoa. We review ourwork on descriptive embryology and studies of selected transcription factor gene families, where our

knowledge from **Acropora** is particularly advanced relative to other cnidarians. We also describe a recent preliminary whole genome initiative, a coral EST database.

ACCESSION NUMBER: 2002392863 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 12141456  
TITLE: Coral development: from classical embryology to molecular control.  
AUTHOR: Ball Eldon E; Hayward David C; Reece-Hoyes John S; Hislop Nikki R; Samuel Gabrielle; Saint Robert; Harrison Peter L; Miller David J  
CORPORATE SOURCE: Research School of Biological Sciences, Australian National University, Canberra, Australian Capital Territory..  
eldon.ball@anu.edu.au  
SOURCE: International journal of developmental biology, (2002) 46 (4) 671-8. Ref: 38  
Journal code: 8917470. ISSN: 0214-6282.  
PUB. COUNTRY: Spain  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
General Review; (REVIEW)  
(REVIEW, TUTORIAL)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 200302  
ENTRY DATE: Entered STN: 20020727  
Last Updated on STN: 20030227  
Entered Medline: 20030226

L5 ANSWER 13 OF 28 MEDLINE on STN

TI Hybridization and the evolution of reef coral diversity.

AB Hundreds of coral species coexist sympatrically on reefs, reproducing in mass-spawning events where hybridization appears common. In the Caribbean, **DNA** sequence data from all three sympatric **Acropora** corals show that mass spawning does not erode species barriers. Species *A. cervicornis* and *A. palmata* are distinct at two nuclear loci or share ancestral alleles. Morphotypes historically given the name **Acropora** *prolifera* are entirely F(1) hybrids of these two species, showing morphologies that depend on which species provides the egg for hybridization. Although selection limits the evolutionary potential of hybrids, F(1) individuals can reproduce asexually and form long-lived, potentially immortal hybrids with unique morphologies.

ACCESSION NUMBER: 2002323266 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 12065836  
TITLE: Hybridization and the evolution of reef coral diversity.  
COMMENT: Comment in: Science. 2002 Dec 13;298(5601):2130-1; author reply 2130-1. PubMed ID: 12481784  
Comment in: Science. 2002 Jun 14;296(5575):1949-50. PubMed ID: 12065810  
AUTHOR: Vollmer Steven V; Palumbi Stephen R  
CORPORATE SOURCE: Department of Organismic and Evolutionary Biology, Harvard University, 16 Divinity Avenue, Cambridge, MA 02138, USA..  
svollmer@oeb.harvard.edu  
SOURCE: Science, (2002 Jun 14) 296 (5575) 2023-5.  
Journal code: 0404511. ISSN: 1095-9203.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 200207  
ENTRY DATE: Entered STN: 20020615  
Last Updated on STN: 20021231  
Entered Medline: 20020715

L5 ANSWER 14 OF 28 MEDLINE on STN

TI Conservation of a DPP/BMP signaling pathway in the nonbilateral cnidarian

**Acropora millepora.**

AB Members of the TGF-beta superfamily of signaling molecules are widespread in metazoans, but the evolutionary origin of particular subclasses of signaling mechanisms is poorly defined. The DPP/BMP class, for example, is implicated in dorsal-ventral patterning, neural patterning, and limb development. Here we report the presence of several components of a DPP/BMP-specific signal transduction cascade in a nonbilateral animal, the coral **Acropora millepora**. The discovery of these components, a putative type I receptor and two putative receptor-activated Smads, suggests that DPP/BMP signaling predates both dorsal-ventral pattern formation and limb development. We postulate that an ancestral role in neuroepithelial patterning may account for the high level of conservation between DPP/BMP signaling components found in this nonbilateral animal and the more complex triploblastic organisms of the arthropod and chordate phyla.

ACCESSION NUMBER: 2002026363 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 11478521  
TITLE: Conservation of a DPP/BMP signaling pathway in the nonbilateral cnidarian **Acropora millepora**.  
AUTHOR: Samuel G; Miller D; Saint R  
CORPORATE SOURCE: Centre for the Molecular Genetics of Development and Dept. of Molecular Biosciences, Adelaide University, SA, Australia.  
SOURCE: Evolution & development, (2001 Jul-Aug) 3 (4) 241-50.  
Journal code: 100883432. ISSN: 1520-541X.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
OTHER SOURCE: GENBANK-U77639  
ENTRY MONTH: 200112  
ENTRY DATE: Entered STN: 20020121  
Last Updated on STN: 20020121  
Entered Medline: 20011221

L5 ANSWER 15 OF 28 MEDLINE on STN

TI The evolution of nuclear receptors: evidence from the coral **Acropora**.

AB We have amplified and sequenced PCR products derived from 10 nuclear receptor (NR) genes from the anthozoan cnidarian **Acropora millepora**, including five products corresponding to genes not previously reported from the phylum Cnidaria. cDNAs corresponding to seven of these products were sequenced and at least three encode full-length proteins, increasing the number of complete cnidarian NR coding sequences from one to four. All clear orthologs of **Acropora** NRs either lack an activation domain or lack a known ligand, consistent with the idea that the ancestral nuclear receptor was without a ligand. Phylogenetic analyses indicate that most, and possibly all, presently identified cnidarian NRs are members of NR subfamily 2, suggesting that the common ancestor of all known nuclear receptors most resembled members of this subfamily.

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ACCESSION NUMBER: 2001558273 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 11603940  
TITLE: The evolution of nuclear receptors: evidence from the coral **Acropora**.  
AUTHOR: Grasso L C; Hayward D C; Trueman J W; Hardie K M; Janssens P A; Ball E E  
CORPORATE SOURCE: Research School of Biological Sciences, Australian National University, Canberra, ACT 2601, Australia.  
SOURCE: Molecular phylogenetics and evolution, (2001 Oct) 21 (1) 93-102.  
Journal code: 9304400. ISSN: 1055-7903.  
PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 200112  
ENTRY DATE: Entered STN: 20011018  
Last Updated on STN: 20020122  
Entered Medline: 20011205

L5 ANSWER 16 OF 28 MEDLINE on STN

TI Patterns of coral-dinoflagellate associations in **Acropora**: significance of local availability and physiology of Symbiodinium strains and host-symbiont selectivity.

AB Like other reef-building corals, members of the genus **Acropora** form obligate endosymbioses with dinoflagellates (zooxanthellae) belonging to the genus Symbiodinium. Both Symbiodinium and its hosts are diverse assemblages, and the relationships between host and algal genotypes are unclear. In this study, we determined phylogenetic relationships between Symbiodinium isolates from a wide range of **Acropora** species and plotted the algal genotypes onto a molecular phylogeny of 28 **Acropora** species, using the same samples for the host and symbiont genotyping. In addition, we performed a preliminary survey of zooxanthella distribution in **Acropora** species from the central Great Barrier Reef. Three of the four known major zooxanthellae clades were represented in the 168 samples examined, and within the major clade C, three distinct subclades were identified. No evidence was found for coevolution, but several clear patterns of specificity were identified. Moreover, composition of the zooxanthella pool varied among locales and in one host species we found light-related patterns of zooxanthella distribution.

ACCESSION NUMBER: 2001479489 MEDLINE

DOCUMENT NUMBER: PubMed ID: 11522193

TITLE: Patterns of coral-dinoflagellate associations in **Acropora**: significance of local availability and physiology of Symbiodinium strains and host-symbiont selectivity.

COMMENT: Erratum in: Proc R Soc Lond B Biol Sci 2001 Dec 22;268(1485):2617

AUTHOR: van Oppen M J; Palstra F P; Piquet A M; Miller D J

CORPORATE SOURCE: Discipline of Biochemistry and Molecular Biology, James Cook University, Townsville 4811, Australia..  
madeleine.vanoppen@jcu.edu.au

SOURCE: Proceedings of the Royal Society of London. Series B. Biological sciences, (2001 Sep 7) 268 (1478) 1759-67.  
Journal code: 7505889. ISSN: 0962-8452.

PUB. COUNTRY: England: United Kingdom

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200112

ENTRY DATE: Entered STN: 20010828

Last Updated on STN: 20020619

Entered Medline: 20011207

L5 ANSWER 17 OF 28 MEDLINE on STN

TI The evolutionary history of the coral genus **Acropora** (Scleractinia, Cnidaria) based on a mitochondrial and a nuclear marker: reticulation, incomplete lineage sorting, or morphological convergence?.

AB This study examines molecular relationships across a wide range of species in the mass spawning scleractinian coral genus **Acropora**. Molecular phylogenies were obtained for 28 species using DNA sequence analyses of two independent markers, a nuclear intron and the mtDNA putative control region. Although the compositions of the major clades in the phylogenies based on these two markers were similar, there were several important differences. This, in combination with the fact

that many species were not monophyletic, suggests either that introgressive hybridization is occurring or that lineage sorting is incomplete. The molecular tree topologies bear little similarity to the results of a recent cladistic analysis based on skeletal morphology and are at odds with the fossil record. We hypothesize that these conflicting results may be due to the same morphology having evolved independently more than once in *Acropora* and/or the occurrence of extensive interspecific hybridization and introgression in combination with morphology being determined by a small number of genes. Our results indicate that many *Acropora* species belong to a species complex or syngameon and that morphology has little predictive value with regard to syngameon composition. Morphological species in the genus often do not correspond to genetically distinct evolutionary units. Instead, species that differ in timing of gamete release tend to constitute genetically distinct clades.

ACCESSION NUMBER: 2001359782 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 11420370  
TITLE: The evolutionary history of the coral genus *Acropora* (Scleractinia, Cnidaria) based on a mitochondrial and a nuclear marker: reticulation, incomplete lineage sorting, or morphological convergence?.  
AUTHOR: van Oppen M J; McDonald B J; Willis B; Miller D J  
CORPORATE SOURCE: Biochemistry and Molecular Biolog, James Cook University, Townsville, Australia.. madeleine.vanoppen@jcu.edu.au  
SOURCE: Molecular biology and evolution, (2001 Jul) 18 (7) 1315-29. Journal code: 8501455. ISSN: 0737-4038.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 200109  
ENTRY DATE: Entered STN: 20011001  
Last Updated on STN: 20011001  
Entered Medline: 20010927

L5 ANSWER 18 OF 28 MEDLINE on STN

TI Assessing coral stress responses using molecular biomarkers of gene transcription.

AB We present a method for detecting rapid changes in coral gene expression at the messenger ribonucleic acid (mRNA) level. The staghorn coral *Acropora cervicornis* was exposed to 1 and 10 microg/L permethrin and 25 and 50 microg/L copper for 4 h. Using differential display polymerase chain reaction (PCR), mRNA associated with each toxicant exposure were reverse transcribed into complementary DNA (cDNA) fragments that were subsequently amplified and isolated. Six differentially expressed cDNA fragments were further developed into molecular probes that were used in Northern dot blots to determine the change in transcription levels of target transcripts. Changes in mRNA abundance were quantified by densitometry of chemiluminescence of digoxigenin-labeled probes hybridizing to target mRNA transcripts. The six gene probes showed varying degrees of sensitivity to the toxicants as well as specificity between toxicants. These probes were hybridized in Southern blots to genomic DNA from *A. formosa* sperm, which lacks zooxanthellae, to demonstrate that the genes coding for the mRNA transcripts produced are found within the coral genome. The gene probes developed in this study provide coral biologists with a new tool for coral assessment. Gene probes are sensitive, toxicant-specific biomarkers of coral stress responses with which gene sequence information can be obtained, providing a mechanism for identifying the stressor altering the gene expression.

ACCESSION NUMBER: 2001251362 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 11349854  
TITLE: Assessing coral stress responses using molecular biomarkers of gene transcription.

AUTHOR: Morgan M B; Vogelien D L; Snell T W  
 CORPORATE SOURCE: Georgia Institute of Technology, School of Biology, Atlanta  
 30332-0230, USA.. gt3099b@prism.gatech.edu  
 SOURCE: Environmental toxicology and chemistry / SETAC, (2001 Mar)  
 20 (3) 537-43.  
 Journal code: 8308958. ISSN: 0730-7268.  
 PUB. COUNTRY: United States  
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
 LANGUAGE: English  
 FILE SEGMENT: Priority Journals  
 ENTRY MONTH: 200106  
 ENTRY DATE: Entered STN: 20010611  
 Last Updated on STN: 20010611  
 Entered Medline: 20010607

L5 ANSWER 19 OF 28 MEDLINE on STN

TI Examination of species boundaries in the **Acropora** cervicornis  
 group (Scleractinia, cnidaria) using nuclear **DNA** sequence  
 analyses.

AB Although **Acropora** is the most species-rich genus of the  
 scleractinian (stony) corals, only three species occur in the Caribbean:  
 A. cervicornis, A. palmata and A. prolifera. Based on overall coral  
 morphology, abundance and distribution patterns, it has been suggested  
 that A. prolifera may be a hybrid between A. cervicornis and A. palmata.  
 The species boundaries among these three morphospecies were examined using  
**DNA** sequence analyses of the nuclear Pax-C 46/47 intron and the  
 ribosomal **DNA** Internal Transcribed Spacer (ITS1 and ITS2) and  
 5.8S regions. Moderate levels of sequence variability were observed in  
 the ITS and 5.8S sequences (up to 5.2% overall sequence difference), but  
 variability within species was as large as between species and all three  
 species carried similar sequences. Since this is unlikely to represent a  
 shared ancestral polymorphism, the data suggest that introgressive  
 hybridization occurs among the three species. For the Pax-C intron, A.  
 cervicornis and A. palmata had very distinct allele frequencies and A.  
 cervicornis carried a unique allele at a frequency of 0.769 (although  
 sequence differences between alleles were small). All A. prolifera  
 colonies examined were heterozygous for the Pax-C intron, whereas  
 heterozygosity was only 0.286 and 0.333 for A. cervicornis and A. palmata,  
 respectively. These data support the hypothesis that A. prolifera is the  
 product of hybridization between two species that have a different allelic  
 composition for the Pax-C intron, i.e. A. cervicornis and A. palmata. We  
 therefore suggest that A. prolifera is a hybrid between A. cervicornis and  
 A. palmata, which backcrosses with the parental species at low frequency.

ACCESSION NUMBER: 2001009950 MEDLINE

DOCUMENT NUMBER: PubMed ID: 10972775

TITLE: Examination of species boundaries in the **Acropora**  
 cervicornis group (Scleractinia, cnidaria) using nuclear  
**DNA** sequence analyses.

AUTHOR: Oppen M J; Willis B L; Vugt H W; Miller D J

CORPORATE SOURCE: Biochemistry and Molecular Biology and Marine Biology, James  
 Cook University, Townsville 4811, Australia..  
 Madeleine.vanOppen@jcu.edu.au

SOURCE: Molecular ecology, (2000 Sep) 9 (9) 1363-73.  
 Journal code: 9214478. ISSN: 0962-1083.

PUB. COUNTRY: ENGLAND: United Kingdom

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF239046; GENBANK-AF239047; GENBANK-AF239048;  
 GENBANK-AF239049; GENBANK-AF239050; GENBANK-AF239051;  
 GENBANK-AF239052; GENBANK-AF239053; GENBANK-AF239054;  
 GENBANK-AF239055; GENBANK-AF239056; GENBANK-AF239057;  
 GENBANK-AF239058; GENBANK-AF239059; GENBANK-AF239060;  
 GENBANK-AF239061; GENBANK-AF239062; GENBANK-AF239063;



GENBANK-AF239064; GENBANK-AF239065; GENBANK-AF239066;  
GENBANK-AF239067; GENBANK-AF239068; GENBANK-AF239069;  
GENBANK-AF239070; GENBANK-AF239071; GENBANK-AF239072;  
GENBANK-AF239073; GENBANK-AF239074; GENBANK-AF239075; +

ENTRY MONTH: 200010  
ENTRY DATE: Entered STN: 20010322  
Last Updated on STN: 20010322  
Entered Medline: 20001023

L5 ANSWER 20 OF 28 MEDLINE on STN

TI Gene content and organization in a segment of the mitochondrial genome of the scleractinian coral **Acropora tenuis**: major differences in gene order within the anthozoan subclass zoantharia.

ACCESSION NUMBER: 2000073049 MEDLINE

DOCUMENT NUMBER: PubMed ID: 10605123

TITLE: Gene content and organization in a segment of the mitochondrial genome of the scleractinian coral **Acropora tenuis**: major differences in gene order within the anthozoan subclass zoantharia.

AUTHOR: van Oppen M J; Hislop N R; Hagerman P J; Miller D J

CONTRACT NUMBER: GM 52557 (NIGMS)

SOURCE: Molecular biology and evolution, (1999 Dec) 16 (12) 1812-5.  
Journal code: 8501455. ISSN: 0737-4038.

PUB. COUNTRY: United States

DOCUMENT TYPE: Letter

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200001

ENTRY DATE: Entered STN: 20000209  
Last Updated on STN: 20000209  
Entered Medline: 20000131

*bad date*

L5 ANSWER 21 OF 28 MEDLINE on STN

TI Reproductive and genetic evidence for a reticulate evolutionary history of mass-spawning corals.

AB Reef-building corals, which reproduce through simultaneous multispecies spawning, are thought to hybridize frequently, and it is hypothesized that they have evolved in repeated rounds of species separation and fusion. We conducted cross-fertilization experiments and molecular analyses with a number of mass-spawning coral species in the genus **Acropora**. A high rate of interspecific fertilization occurred between some species despite very different morphologies. The hybrid larvae developed normally and contained an allelic sequence transmitted from each parent, suggesting common diploid hybridization. Molecular phylogenetic analyses provided strong evidence for a gene pool shared between the hybridizing species. These reproductive and genetic characteristics are consistent with a species complex formed under the separation/fusion processes predicted for a reticulate evolutionary history.

ACCESSION NUMBER: 2000022992 MEDLINE

DOCUMENT NUMBER: PubMed ID: 10555292

TITLE: Reproductive and genetic evidence for a reticulate evolutionary history of mass-spawning corals.

AUTHOR: Hatta M; Fukami H; Wang W; Omori M; Shimoike K; Hayashibara T; Ina Y; Sugiyama T

CORPORATE SOURCE: National Institute of Genetics, Mishima, Japan..  
mhatta@lab.nig.ac.jp

SOURCE: Molecular biology and evolution, (1999 Nov) 16 (11) 1607-13.

Journal code: 8501455. ISSN: 0737-4038.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AB009715; GENBANK-AB009716; GENBANK-AB009717;

GENBANK-AB009718; GENBANK-AB009719; GENBANK-AB009720;  
 GENBANK-AB009721; GENBANK-AB009722; GENBANK-AB009723;  
 GENBANK-AB009724; GENBANK-AB009725; GENBANK-AB009726;  
 GENBANK-AB009727; GENBANK-AB009728; GENBANK-AB009729;  
 GENBANK-AB009730; GENBANK-AB009731; GENBANK-AB009732;  
 GENBANK-AB009733; GENBANK-AB009734; GENBANK-AB009735;  
 GENBANK-AB009736; GENBANK-AB009737; GENBANK-AB009738;  
 GENBANK-AB009739; GENBANK-AB009740; GENBANK-AB009741;  
 GENBANK-AB009742; GENBANK-AB009743; GENBANK-AB009744

ENTRY MONTH: 199911  
 ENTRY DATE: Entered STN: 20000111  
 Last Updated on STN: 20000111  
 Entered Medline: 19991123

L5 ANSWER 22 OF 28 MEDLINE on STN

TI Atypically low rate of cytochrome b evolution in the scleractinian coral genus **Acropora**.

AB Unexpectedly low levels of mitochondrial DNA (mtDNA) cytochrome b sequence divergence are found between species of the scleractinian coral genus **Acropora**. Comparison of 964 positions of the cytochrome b gene of two out of the three Caribbean **Acropora** species with seven of their Pacific congeners shows only 0.3-0.8% sequence difference. Species in these biogeographic regions have been evolving independently for at least three million years (since the rise of the Isthmus of Panama) and this geological date is used to estimate nucleotide divergence rates. The results indicate that the **Acropora** cytochrome b gene is evolving at least 10-20 times slower than the 'standard' vertebrate mtDNA clock and is one of the most slowly evolving animal mitochondrial genes described to date. The possibility is discussed that, unlike higher animals, cnidarians may have a functional mtDNA mismatch repair system.

ACCESSION NUMBER: 1999197465 MEDLINE  
 DOCUMENT NUMBER: PubMed ID: 10097392  
 TITLE: Atypically low rate of cytochrome b evolution in the scleractinian coral genus **Acropora**.  
 AUTHOR: van Oppen M J; Willis B L; Miller D J  
 CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, James Cook University, Townsville, Australia.  
 SOURCE: Proceedings of the Royal Society of London. Series B. Biological sciences, (1999 Jan 22) 266 (1415) 179-83. Journal code: 7505889. ISSN: 0962-8452.  
 PUB. COUNTRY: ENGLAND: United Kingdom  
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
 LANGUAGE: English  
 FILE SEGMENT: Priority Journals  
 OTHER SOURCE: GENBANK-AF152244  
 ENTRY MONTH: 199904  
 ENTRY DATE: Entered STN: 19990426  
 Last Updated on STN: 19990426  
 Entered Medline: 19990413

L5 ANSWER 23 OF 28 MEDLINE on STN

TI Pax-6 origins--implications from the structure of two coral pax genes.

AB Vertebrate Pax-6 and its Drosophila homolog eyeless play central roles in eye specification, although it is not clear if this represents the ancestral role of this gene class. As the most "primitive" animals with true nervous systems, the Cnidaria may be informative in terms of the evolution of the Pax gene family. For this reason we surveyed the Pax gene complement of a representative of the basal cnidarian class (the Anthozoa), the coral **Acropora** millepora. cDNAs encoding two coral Pax proteins were isolated. Pax-Aam encoded a protein containing only a paired domain, whereas Pax-Cam also contained a homeodomain clearly related to those in the Pax-6 family. The paired domains in both proteins most resembled the vertebrate Pax-2/5/8 class, but shared several distinctive substitutions. As in most Pax-6 homologs and orthologs, an

intron was present in the Pax-Cam locus at a position corresponding to residues 46/47 in the homeodomain. We propose a model for evolution of the Pax family, in which the ancestor of all of the vertebrate Pax genes most resembled Pax-6, and arose via fusion of a Pax-Aam-like gene (encoding only a paired domain) with an anteriorly-expressed homeobox gene resembling the paired-like class.

ACCESSION NUMBER: 1998384486 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 9716726  
TITLE: Pax-6 origins--implications from the structure of two coral pax genes.  
AUTHOR: Catmull J; Hayward D C; McIntyre N E; Reece-Hoyes J S; Mastro R; Callaerts P; Ball E E; Miller D J  
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, James Cook University, Townsville, Queensland 4811, Australia.  
SOURCE: Development genes and evolution, (1998 Aug) 208 (6) 352-6. Journal code: 9613264. ISSN: 0949-944X.  
PUB. COUNTRY: GERMANY: Germany, Federal Republic of  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199811  
ENTRY DATE: Entered STN: 19990106  
Last Updated on STN: 19990106  
Entered Medline: 19981118

L5 ANSWER 24 OF 28 MEDLINE on STN

TI Variation in the ribosomal internal transcribed spacers and 5.8S rDNA among five species of **Acropora** (Cnidaria; Scleractinia): patterns of variation consistent with reticulate evolution.

AB The ITS sequences of **Acropora** spp. are the shortest so far identified in any metazoan and are among the shortest seen in eukaryotes; ITS1 was 70-80 bases, and ITS2 was 100-112 bases. The ITS sequences were also highly variable, but base composition and secondary structure prediction indicate that divergent sequence variants are unlikely to be pseudogenes. The pattern of variation was unusual in several other respects: (1) two distinct ITS2 types were detected in both *A. hyacinthus* and *A. cytherea*, species known to hybridize in vitro with high success rates, and a putative intermediate ITS2 form was also detected in *A. cytherea*; (2) *A. valida* was found to contain highly (29%) diverged ITS1 variants; and (3) *A. longicyathus* contained two distinct 5.8S rDNA types. These data are consistent with a reticulate evolutionary history for the genus **Acropora**.

ACCESSION NUMBER: 97303600 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 9159924  
TITLE: Variation in the ribosomal internal transcribed spacers and 5.8S rDNA among five species of **Acropora** (Cnidaria; Scleractinia): patterns of variation consistent with reticulate evolution.  
AUTHOR: Odorico D M; Miller D J  
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, James Cook University of North Queensland, Australia.  
SOURCE: Molecular biology and evolution, (1997 May) 14 (5) 465-73. Journal code: 8501455. ISSN: 0737-4038.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
OTHER SOURCE: GENBANK-U82719; GENBANK-U82720; GENBANK-U82721; GENBANK-U82722; GENBANK-U82723; GENBANK-U82724; GENBANK-U82725; GENBANK-U82726; GENBANK-U82727; GENBANK-U82728; GENBANK-U82729; GENBANK-U82730; GENBANK-U82731; GENBANK-U82732; GENBANK-U82733; GENBANK-U82734; GENBANK-U82735; GENBANK-U82736; GENBANK-X53498

ENTRY MONTH: 199707  
ENTRY DATE: Entered STN: 19970721  
Last Updated on STN: 19970721  
Entered Medline: 19970707

L5 ANSWER 25 OF 28 MEDLINE on STN

TI Isolation and characterization of a mini-collagen gene encoding a nematocyst capsule protein from a reef-building coral, **Acropora donei**.

AB Genomic and cDNA clones of a mcol gene encoding mini-collagen (MCOL), a nematocyst capsule protein, have been isolated from a reef-building coral, **Acropora donei** (Anthozoa). The gene and its flanking regions, comprising 5382 bp and covering three exons and two introns, were sequenced. Exons 2 and 3 together have an open reading frame which can encode a MCOL of 176 amino acids (aa). The coral MCOL has all the characteristic regions present in the four hydra MCOL specified by the four mcol cDNA clones previously isolated from *Hydra magnipapillata* (Hydrozoa) by Kurz et al. [J. Cell Biol. 115 (1991) 1159-1169], including a central Gly-Xaa-Yaa region and flanking Pro-rich and Cys-repeat regions. This observation suggests that a mcol family is highly conserved in Anthozoa and Hydrozoa, and also that the characteristic regions present in MCOL are essential for the structure and function of these peptides.

ACCESSION NUMBER: 95137387 MEDLINE

DOCUMENT NUMBER: PubMed ID: 7835699

TITLE: Isolation and characterization of a mini-collagen gene encoding a nematocyst capsule protein from a reef-building coral, **Acropora donei**.

AUTHOR: Wang W; Omori M; Hayashibara T; Shimoike K; Hatta M; Sugiyama T; Fujisawa T

CORPORATE SOURCE: Department of Aquatic Biosciences, Tokyo University of Fisheries, Japan.

SOURCE: Gene, (1995 Jan 23) 152 (2) 195-200.  
Journal code: 7706761. ISSN: 0378-1119.

PUB. COUNTRY: Netherlands

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-D30747

ENTRY MONTH: 199503

ENTRY DATE: Entered STN: 19950314  
Last Updated on STN: 19950314  
Entered Medline: 19950301

L5 ANSWER 26 OF 28 MEDLINE on STN

TI Nucleotide sequence of a cDNA clone encoding the precursor of the peridinin-chlorophyll a-binding protein from the dinoflagellate *Symbiodinium* sp.

AB mRNA from the dinoflagellate *Symbiodinium* sp. isolated from the staghorn coral **Acropora formosa** was used for the construction of cDNA libraries. A cDNA clone was identified which encoded the precursor of peridinin-chlorophyll a-binding protein (PCP), including a 52 amino acid transit peptide and the 313 amino acid mature protein. The deduced amino acid sequence clearly contains an internal duplication, implying that amongst dinoflagellates the M(r) 35,000 form of PCP has arisen by duplication and fusion of genes encoding the M(r) 15,000 form. This is the first reported sequence of a dinoflagellate light-harvesting protein. The anatomy of the mature protein and the transit peptide are discussed.

ACCESSION NUMBER: 94207192 MEDLINE

DOCUMENT NUMBER: PubMed ID: 8155886

TITLE: Nucleotide sequence of a cDNA clone encoding the precursor of the peridinin-chlorophyll a-binding protein from the dinoflagellate *Symbiodinium* sp.

AUTHOR: Norris B J; Miller D J

CORPORATE SOURCE: Department of Molecular Sciences, James Cook University of

SOURCE: North Queensland, Townsville, Australia.  
 Plant molecular biology, (1994 Feb) 24 (4) 673-7.  
 Journal code: 9T06343. ISSN: 0167-4412.  
 PUB. COUNTRY: Netherlands  
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
 LANGUAGE: English  
 FILE SEGMENT: Priority Journals  
 OTHER SOURCE: GENBANK-L13613  
 ENTRY MONTH: 199405  
 ENTRY DATE: Entered STN: 19940526  
 Last Updated on STN: 19940526  
 Entered Medline: 19940516

L5 ANSWER 27 OF 28 MEDLINE on STN

TI Genomes of diploblastic organisms contain homeoboxes: sequence of eveC, an even-skipped homologue from the cnidarian **Acropora** formosa.

AB We report the nucleotide sequence of eveC, a cnidarian eve-class homeobox; this is the first homeobox to be identified in any diploblastic organism, and is only the second eve-class in an invertebrate. Similarity between the predicted amino acid sequence of the eveC homeodomain and its insect and vertebrate equivalents was approximately 75-80% but, in the case of eveC, a role in segmentation can be ruled out. Our findings thus support the 'co-option' hypothesis: homeoboxes were an early feature of metazoan genomes, corresponding to the **DNA**-binding domains of more general transcription factors.

ACCESSION NUMBER: 92335359 MEDLINE

DOCUMENT NUMBER: PubMed ID: 1352890

TITLE: Genomes of diploblastic organisms contain homeoboxes: sequence of eveC, an even-skipped homologue from the cnidarian **Acropora** formosa.

AUTHOR: Miles A; Miller D J

CORPORATE SOURCE: Department of Chemistry and Biochemistry, James Cook University of North Queensland, Townsville, Australia.

SOURCE: Proceedings of the Royal Society of London. Series B. Biological sciences, (1992 May 22) 248 (1322) 159-61.  
 Journal code: 7505889. ISSN: 0962-8452.

PUB. COUNTRY: ENGLAND: United Kingdom

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199208

ENTRY DATE: Entered STN: 19920904

Last Updated on STN: 19970203

Entered Medline: 19920819

L5 ANSWER 28 OF 28 MEDLINE on STN

TI Nucleotide sequences of highly repetitive **DNA** from scleractinian corals.

AB The staghorn coral genome contains 5% of a satellite **DNA**, consisting of 80 to 300 x 10(3) copies of a 118-bp repeat unit per haploid **Acropora** genome.

ACCESSION NUMBER: 90076967 MEDLINE

DOCUMENT NUMBER: PubMed ID: 2574130

TITLE: Nucleotide sequences of highly repetitive **DNA** from scleractinian corals.

AUTHOR: McMillan J; Miller D J

CORPORATE SOURCE: Department of Chemistry and Biochemistry, James Cook University, Townsville, Queensland, Australia.

SOURCE: Gene, (1989 Nov 15) 83 (1) 185-6.  
 Journal code: 7706761. ISSN: 0378-1119.

PUB. COUNTRY: Netherlands

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-M30505; GENBANK-M30506; GENBANK-M30507;  
GENBANK-M30508; GENBANK-M30509  
ENTRY MONTH: 199001  
ENTRY DATE: Entered STN: 19900328  
Last Updated on STN: 19950206  
Entered Medline: 19900116

=> d his

(FILE 'HOME' ENTERED AT 10:16:32 ON 17 AUG 2004)

FILE 'STNGUIDE' ENTERED AT 10:17:29 ON 17 AUG 2004

FILE 'HOME' ENTERED AT 10:17:52 ON 17 AUG 2004

FILE 'MEDLINE' ENTERED AT 10:17:59 ON 17 AUG 2004

L1 0 S ACROPORA+NT/CT  
L2 0 S MONTIPORA+NT/CT  
L3 75 S ACROPORA?  
L4 20 S MONTIPORA?  
L5 28 S L3 AND DNA  
L6 1 S L4 AND DNA

=> l5 and encoding protein

L5 IS NOT A RECOGNIZED COMMAND

The previous command name entered was not recognized by the system.  
For a list of commands available to you in the current file, enter  
"HELP COMMANDS" at an arrow prompt (=>).

=> s l5 and encoding protein

99704 ENCODING

1298601 PROTEIN

270 ENCODING PROTEIN

(ENCODING(W) PROTEIN)

L7 0 L5 AND ENCODING PROTEIN

=> s l5 and protein

1298601 PROTEIN

L8 9 L5 AND PROTEIN

=> d l8 ti abs ibib tot

L8 ANSWER 1 OF 9 MEDLINE on STN

TI Mutational analysis of the **Acropora** millepora PaxD paired domain  
highlights the importance of the linker region for **DNA** binding.

AB Pax transcription factors are found in animals, from simple sponges to  
insects and vertebrates. The defining feature of Pax proteins is the  
**DNA**-binding paired domain (PD), which consists of two  
helix-turn-helix subdomains, joined with a linker region. Despite high  
specificity in vivo, the paired domains of different Pax proteins bind  
similar consensus **DNA** sequences in vitro. Using bandshift  
techniques, we show here that the paired domain of the **Acropora**  
millepora PaxD **protein**, which unambiguously belongs to the  
Pax3/7 group, does not bind to three defined paired domain-binding sites.  
Domain swapping experiments and site-directed mutagenesis identified two  
amino acid residues in the linker region of the paired domain as critical  
to **DNA** binding; G70 and S71 are highly conserved in Pax  
proteins, but differ in PaxD (L70 and N71). The PaxD data thus highlight  
the importance of the linker region, and particularly G70 and S71, in  
**DNA** binding by Pax proteins.

ACCESSION NUMBER: 2003519437 MEDLINE

DOCUMENT NUMBER: PubMed ID: 14597391

TITLE: Mutational analysis of the **Acropora** millepora

PaxD paired domain highlights the importance of the linker region for **DNA** binding.

AUTHOR: Nordstrom Karin; Scholten Ingo; Nordstrom Johanna; Larhammar Dan; Miller David

CORPORATE SOURCE: Department of Neuroscience, Pharmacology, Uppsala University, Box 593, Uppsala 751 24, Sweden.. Karin.Nordstrom@cob.lu.se

SOURCE: Gene, (2003 Nov 27) 320 81-7. Journal code: 7706761. ISSN: 0378-1119.

PUB. COUNTRY: Netherlands

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200401

ENTRY DATE: Entered STN: 20031105  
Last Updated on STN: 20040128  
Entered Medline: 20040127

L8 ANSWER 2 OF 9 MEDLINE on STN

TI **DNA**-binding characteristics of cnidarian Pax-C and Pax-B proteins in vivo and in vitro: no simple relationship with the Pax-6 and Pax-2/5/8 classes.

AB Cnidarians are the simplest animals in which distinct eyes are present. We have previously suggested that cnidarian Pax-Cam might represent a precursor of the Pax-6 class. Here we show that when expressed in Drosophila imaginal discs, Pax-Cam chimeric proteins containing the C-terminal region of EY were capable of eye induction and driving expression of a reporter gene under the control of a known EY target (the sine oculis gene). Whilst these results are consistent with a Pax-6-like function for Pax-Cam, in band shift experiments we were unable to distinguish the **DNA**-binding behaviour of the Pax-Cam Paired domain from that of a second **Acropora Pax protein**, Pax-Bam. The ability of a Pax-Bam/EY chimera to also induce eye formation in leg imaginal discs, together with the in vitro data, cast doubt on previously assumed direct relationships between cnidarian Pax genes and the Pax-6 and Pax-2/5/8 classes of bilateral animals.  
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ACCESSION NUMBER: 2003447306 MEDLINE

DOCUMENT NUMBER: PubMed ID: 14508814

TITLE: **DNA**-binding characteristics of cnidarian Pax-C and Pax-B proteins in vivo and in vitro: no simple relationship with the Pax-6 and Pax-2/5/8 classes.

AUTHOR: Plaza Serge; De Jong Danielle M; Gehring Walter J; Miller David J

CORPORATE SOURCE: Biozentrum, University of Basel, CH-4056 Basel, Switzerland.

SOURCE: Journal of experimental zoology. Part B. Molecular and developmental evolution, (2003 Oct 15) 299 (1) 26-35. Journal code: 101168228.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200312

ENTRY DATE: Entered STN: 20030926  
Last Updated on STN: 20031218  
Entered Medline: 20031204

L8 ANSWER 3 OF 9 MEDLINE on STN

TI A DM domain **protein** from a coral, **Acropora millepora**, homologous to proteins important for sex determination.

AB The identification and functional studies of DM domain-containing proteins Doublesex, MAB-3, and DMRT1 indicated that flies, nematodes, and humans share at least some of the molecular mechanisms of sex determination. We

identified a gene, AmDM1, from the coral **Acropora** millepora that encodes a homologous DM domain-containing **protein**. Molecular analyses show that the AmDM1 primary transcript is processed to generate four different messenger RNAs. Alternative use of two polyadenylation sites produces transcripts that vary only in the 3' untranslated regions, whereas alternative splicing generates transcripts with and without the region coding for the DM domain. All the transcripts include a second motif, the DMA domain, which is found in a number of other proteins containing a DM domain. Hermaphroditic *A. millepora* differentiates sexual cells seasonally before the spring spawn, and Northern blot analysis shows that the AmDM1 transcripts are present at higher levels during sexual differentiation. The non-DM domain-containing messages are also present at significant levels in late embryos, but DM domain transcripts are extremely rare at this stage. These data suggest that the association of DM domain proteins and sexual determination or differentiation predates the separation of the Cnidaria from the rest of the Metazoa.

ACCESSION NUMBER: 2003230931 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 12752764  
TITLE: A DM domain **protein** from a coral,  
**Acropora** millepora, homologous to proteins  
important for sex determination.  
AUTHOR: Miller Steven W; Hayward David C; Bunch Thomas A; Miller  
David J; Ball Eldon E; Bardwell Vivian J; Zarkower David;  
Brower Danny L  
CORPORATE SOURCE: Departments of Molecular and Cellular Biology and  
Biochemistry, University of Arizona, Tucson, AZ 85721, USA.  
CONTRACT NUMBER: GM42474 (NIGMS)  
GM59152 (NIGMS)  
SOURCE: Evolution & development, (2003 May-Jun) 5 (3) 251-8.  
Journal code: 100883432. ISSN: 1520-541X.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 200312  
ENTRY DATE: Entered STN: 20030520  
Last Updated on STN: 20031230  
Entered Medline: 20031229

L8 ANSWER 4 OF 9 MEDLINE on STN

TI The mitochondrial genome of **Acropora** tenuis (Cnidaria;  
Scleractinia) contains a large group I intron and a candidate control  
region.

AB The complete nucleotide sequence of the mitochondrial genome of the coral  
**Acropora** tenuis has been determined. The 18,338 bp *A. tenuis*  
mitochondrial genome contains the standard metazoan complement of 13  
**protein**-coding and two rRNA genes, but only the same two tRNA  
genes (trnM and trnW) as are present in the mtDNA of the sea anemone,  
Metridium senile. The *A. tenuis* nad5 gene is interrupted by a large group  
I intron which contains ten **protein**-coding genes and rns; *M.*  
senile has an intron at the same position but this contains only two  
**protein**-coding genes. Despite the large distance (about 11.5 kb)  
between the 5'-exon and 3'-exon boundaries, the *A. tenuis* nad5 gene is  
functional, as we were able to RT-PCR across the predicted intron splice  
site using total RNA from *A. tenuis*. As in *M. senile*, all of the genes in  
the *A. tenuis* mt genome have the same orientation, but their organization  
is completely different in these two zoantharians: The only common gene  
boundaries are those at each end of the group I intron and between trnM  
and rnl. Finally, we provide evidence that the rns-cox3 intergenic region  
in *A. tenuis* may correspond to the mitochondrial control region of higher  
animals. This region contains repetitive elements, and has the potential  
to form secondary structures of the type characteristic of vertebrate  
D-loops. Comparisons between a wide range of **Acropora** species  
showed that a long hairpin predicted in rns-cox3 is phylogenetically



conserved, and allowed the tentative identification of conserved sequence blocks.

ACCESSION NUMBER: 2002409827 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 12165838  
TITLE: The mitochondrial genome of *Acropora tenuis*  
(Cnidaria; Scleractinia) contains a large group I intron  
and a candidate control region.  
AUTHOR: van Oppen Madeleine J H; Catmull Julian; McDonald Brenda J;  
Hislop Nikki R; Hagerman Paul J; Miller David J  
CORPORATE SOURCE: Biochemistry and Molecular Biology, James Cook University,  
Townsville, Queensland 4811, Australia.  
CONTRACT NUMBER: GM35305 (NIGMS)  
SOURCE: Journal of molecular evolution, (2002 Jul) 55 (1) 1-13.  
Journal code: 0360051. ISSN: 0022-2844.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 200302  
ENTRY DATE: Entered STN: 20020808  
Last Updated on STN: 20030205  
Entered Medline: 20030204

L8 ANSWER 5 OF 9 MEDLINE on STN

TI Conservation of a DPP/BMP signaling pathway in the nonbilateral cnidarian  
*Acropora millepora*.

AB Members of the TGF-beta superfamily of signaling molecules are widespread  
in metazoans, but the evolutionary origin of particular subclasses of  
signaling mechanisms is poorly defined. The DPP/BMP class, for example,  
is implicated in dorsal-ventral patterning, neural patterning, and limb  
development. Here we report the presence of several components of a  
DPP/BMP-specific signal transduction cascade in a nonbilateral animal, the  
coral *Acropora millepora*. The discovery of these components, a  
putative type I receptor and two putative receptor-activated Smads,  
suggests that DPP/BMP signaling predates both dorsal-ventral pattern  
formation and limb development. We postulate that an ancestral role in  
neuroepithelial patterning may account for the high level of conservation  
between DPP/BMP signaling components found in this nonbilateral animal and  
the more complex triploblastic organisms of the arthropod and chordate  
phyla.

ACCESSION NUMBER: 2002026363 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 11478521  
TITLE: Conservation of a DPP/BMP signaling pathway in the  
nonbilateral cnidarian *Acropora millepora*.  
AUTHOR: Samuel G; Miller D; Saint R  
CORPORATE SOURCE: Centre for the Molecular Genetics of Development and Dept.  
of Molecular Biosciences, Adelaide University, SA,  
Australia.  
SOURCE: Evolution & development, (2001 Jul-Aug) 3 (4) 241-50.  
Journal code: 100883432. ISSN: 1520-541X.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
OTHER SOURCE: GENBANK-U77639  
ENTRY MONTH: 200112  
ENTRY DATE: Entered STN: 20020121  
Last Updated on STN: 20020121  
Entered Medline: 20011221

L8 ANSWER 6 OF 9 MEDLINE on STN

TI Pax-6 origins--implications from the structure of two coral pax genes.

AB Vertebrate Pax-6 and its *Drosophila* homolog eyeless play central roles in  
eye specification, although it is not clear if this represents the

ancestral role of this gene class. As the most "primitive" animals with true nervous systems, the Cnidaria may be informative in terms of the evolution of the Pax gene family. For this reason we surveyed the Pax gene complement of a representative of the basal cnidarian class (the Anthozoa), the coral **Acropora** millepora. cDNAs encoding two coral Pax proteins were isolated. Pax-Aam encoded a **protein** containing only a paired domain, whereas Pax-Cam also contained a homeodomain clearly related to those in the Pax-6 family. The paired domains in both proteins most resembled the vertebrate Pax-2/5/8 class, but shared several distinctive substitutions. As in most Pax-6 homologs and orthologs, an intron was present in the Pax-Cam locus at a position corresponding to residues 46/47 in the homeodomain. We propose a model for evolution of the Pax family, in which the ancestor of all of the vertebrate Pax genes most resembled Pax-6, and arose via fusion of a Pax-Aam-like gene (encoding only a paired domain) with an anteriorly-expressed homeobox gene resembling the paired-like class.

ACCESSION NUMBER: 1998384486 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 9716726  
TITLE: Pax-6 origins--implications from the structure of two coral pax genes.  
AUTHOR: Catmull J; Hayward D C; McIntyre N E; Reece-Hoyes J S; Mastro R; Callaerts P; Ball E E; Miller D J  
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, James Cook University, Townsville, Queensland 4811, Australia.  
SOURCE: Development genes and evolution, (1998 Aug) 208 (6) 352-6. Journal code: 9613264. ISSN: 0949-944X.  
PUB. COUNTRY: GERMANY: Germany, Federal Republic of  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199811  
ENTRY DATE: Entered STN: 19990106  
Last Updated on STN: 19990106  
Entered Medline: 19981118

L8 ANSWER 7 OF 9 MEDLINE on STN

TI Isolation and characterization of a mini-collagen gene encoding a nematocyst capsule **protein** from a reef-building coral, **Acropora** donei.

AB Genomic and cDNA clones of a mcol gene encoding mini-collagen (MCOL), a nematocyst capsule **protein**, have been isolated from a reef-building coral, **Acropora** donei (Anthozoa). The gene and its flanking regions, comprising 5382 bp and covering three exons and two introns, were sequenced. Exons 2 and 3 together have an open reading frame which can encode a MCOL of 176 amino acids (aa). The coral MCOL has all the characteristic regions present in the four hydra MCOL specified by the four mcol cDNA clones previously isolated from Hydra magnipapillata (Hydrozoa) by Kurz et al. [J. Cell Biol. 115 (1991) 1159-1169], including a central Gly-Xaa-Yaa region and flanking Pro-rich and Cys-repeat regions. This observation suggests that a mcol family is highly conserved in Anthozoa and Hydrozoa, and also that the characteristic regions present in MCOL are essential for the structure and function of these peptides.

ACCESSION NUMBER: 95137387 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 7835699  
TITLE: Isolation and characterization of a mini-collagen gene encoding a nematocyst capsule **protein** from a reef-building coral, **Acropora** donei.  
AUTHOR: Wang W; Omori M; Hayashibara T; Shimoike K; Hatta M; Sugiyama T; Fujisawa T  
CORPORATE SOURCE: Department of Aquatic Biosciences, Tokyo University of Fisheries, Japan.  
SOURCE: Gene, (1995 Jan 23) 152 (2) 195-200. Journal code: 7706761. ISSN: 0378-1119.  
PUB. COUNTRY: Netherlands

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
OTHER SOURCE: GENBANK-D30747  
ENTRY MONTH: 199503  
ENTRY DATE: Entered STN: 19950314  
Last Updated on STN: 19950314  
Entered Medline: 19950301

L8 ANSWER 8 OF 9 MEDLINE on STN

TI Nucleotide sequence of a cDNA clone encoding the precursor of the peridinin-chlorophyll a-binding **protein** from the dinoflagellate *Symbiodinium* sp.  
AB mRNA from the dinoflagellate *Symbiodinium* sp. isolated from the staghorn coral *Acropora formosa* was used for the construction of cDNA libraries. A cDNA clone was identified which encoded the precursor of peridinin-chlorophyll a-binding **protein** (PCP), including a 52 amino acid transit peptide and the 313 amino acid mature **protein**. The deduced amino acid sequence clearly contains an internal duplication, implying that amongst dinoflagellates the M(r) 35,000 form of PCP has arisen by duplication and fusion of genes encoding the M(r) 15,000 form. This is the first reported sequence of a dinoflagellate light-harvesting **protein**. The anatomy of the mature **protein** and the transit peptide are discussed.

ACCESSION NUMBER: 94207192 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 8155886  
TITLE: Nucleotide sequence of a cDNA clone encoding the precursor of the peridinin-chlorophyll a-binding **protein** from the dinoflagellate *Symbiodinium* sp.  
AUTHOR: Norris B J; Miller D J  
CORPORATE SOURCE: Department of Molecular Sciences, James Cook University of North Queensland, Townsville, Australia.  
SOURCE: Plant molecular biology, (1994 Feb) 24 (4) 673-7.  
Journal code: 9106343. ISSN: 0167-4412.  
PUB. COUNTRY: Netherlands  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
OTHER SOURCE: GENBANK-L13613  
ENTRY MONTH: 199405  
ENTRY DATE: Entered STN: 19940526  
Last Updated on STN: 19940526  
Entered Medline: 19940516

L8 ANSWER 9 OF 9 MEDLINE on STN

TI Genomes of diploblastic organisms contain homeoboxes: sequence of eveC, an even-skipped homologue from the cnidarian *Acropora formosa*.  
AB We report the nucleotide sequence of eveC, a cnidarian eve-class homeobox; this is the first homeobox to be identified in any diploblastic organism, and is only the second eve-class in an invertebrate. Similarity between the predicted amino acid sequence of the eveC homeodomain and its insect and vertebrate equivalents was approximately 75-80% but, in the case of eveC, a role in segmentation can be ruled out. Our findings thus support the 'co-option' hypothesis: homeoboxes were an early feature of metazoan genomes, corresponding to the DNA-binding domains of more general transcription factors.

ACCESSION NUMBER: 92335359 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 1352890  
TITLE: Genomes of diploblastic organisms contain homeoboxes: sequence of eveC, an even-skipped homologue from the cnidarian *Acropora formosa*.  
AUTHOR: Miles A; Miller D J  
CORPORATE SOURCE: Department of Chemistry and Biochemistry, James Cook University of North Queensland, Townsville, Australia.

SOURCE: Proceedings of the Royal Society of London. Series B.  
Biological sciences, (1992 May 22) 248 (1322) 159-61.  
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470673 ISOLATED  
756893 DNA  
593 ISOLATED DNA  
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